

RAW SEQUENCE LISTING

EFS

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Application Serial Number: 10/574,770
Source: IFWP
Date Processed by STIC: 3/15/07

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IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/574,770

DATE: 03/15/2007

TIME: 14:41:48

Input Set : N:\efs\03_15_07\10574770_efs\seqlistforfiling.TXT
 Output Set: N:\CRF4\03152007\J574770.raw

4 <110> APPLICANT: McCullough, Karen
 5 Ide, Susan
 6 Lavedan, Christian
 8 <120> TITLE OF INVENTION: USE OF GENETIC POLYMORPHISMS THAT
 9 ASSOCIATE WITH EFFICACY OF TREATMENT OF INFLAMMATORY DISEASE
 12 <130> FILE REFERENCE: 33389 US-PCT
 14 <140> CURRENT APPLICATION NUMBER: 10/574,770
 15 <141> CURRENT FILING DATE: 2006-04-06
 17 <150> PRIOR APPLICATION NUMBER: 60/508,971
 18 <151> PRIOR FILING DATE: 2003-10-06
 20 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/011124
 21 <151> PRIOR FILING DATE: 2005-05-06
 23 <160> NUMBER OF SEQ ID NOS: 22
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 53
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: variation
 34 <222> LOCATION: (1)...(53)
 35 <223> OTHER INFORMATION: TNF locus variant (T at position -1031)
 37 <221> NAME/KEY: variation
 38 <222> LOCATION: (23)...(0)
 39 <223> OTHER INFORMATION: T
 W--> 41 <400> 1
 42 agcaaaggag aagctgagaa gatgaaggaa aagtcaagggt ctggagggc ggg 53
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 53
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Homo sapiens
 49 <220> FEATURE:
 50 <221> NAME/KEY: variation
 51 <222> LOCATION: (1)...(53)
 52 <223> OTHER INFORMATION: TNF locus variant (C at position -1031)
 54 <221> NAME/KEY: variation
 55 <222> LOCATION: (23)...(0)
 56 <223> OTHER INFORMATION: C
 W--> 58 <400> 2
 59 agcaaaggag aagctgagaa gacgaaggaa aagtcaagggt ctggagggc ggg 53
 61 <210> SEQ ID NO: 3
 62 <211> LENGTH: 48
 63 <212> TYPE: DNA

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64 <213> ORGANISM: Homo sapiens
 66 <220> FEATURE:
 67 <221> NAME/KEY: variation
 68 <222> LOCATION: (1)...(48)
 69 <223> OTHER INFORMATION: LTA locus variant (C)
 71 <221> NAME/KEY: variation
 72 <222> LOCATION: (20)...(0)
 73 <223> OTHER INFORMATION: C
 W--> 75 <400> 3
 76 gtgagcagca ggttttagggc tgctgtgggc aagatgcattttgggtg 48
 78 <210> SEQ ID NO: 4
 79 <211> LENGTH: 48
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Homo sapiens
 83 <220> FEATURE:
 84 <221> NAME/KEY: variation
 85 <222> LOCATION: (1)...(48)
 86 <223> OTHER INFORMATION: LTA locus variant (A; ASN60THR)
 88 <221> NAME/KEY: variation
 89 <222> LOCATION: (20)...(0)
 90 <223> OTHER INFORMATION: A
 W--> 92 <400> 4
 93 gtgagcagca ggttttagggc tgctgtgggc aagatgcattttgggtg 48
 95 <210> SEQ ID NO: 5
 96 <211> LENGTH: 50
 97 <212> TYPE: DNA
 98 <213> ORGANISM: Homo sapiens
 100 <220> FEATURE:
 101 <221> NAME/KEY: variation
 102 <222> LOCATION: (1)...(50)
 103 <223> OTHER INFORMATION: CCR2 locus variant (G)
 105 <221> NAME/KEY: variation
 106 <222> LOCATION: (10)...(0)
 107 <223> OTHER INFORMATION: G
 W--> 109 <400> 5
 110 atgctggtcg tcctcatctt aataaactgc aaaaagctga agtgcttgac 50
 112 <210> SEQ ID NO: 6
 113 <211> LENGTH: 50
 114 <212> TYPE: DNA
 115 <213> ORGANISM: Homo sapiens
 117 <220> FEATURE:
 118 <221> NAME/KEY: variation
 119 <222> LOCATION: (1)...(50)
 120 <223> OTHER INFORMATION: CCR2 locus variant (A; VAL64ILE)
 122 <221> NAME/KEY: variation
 123 <222> LOCATION: (10)...(0)
 124 <223> OTHER INFORMATION: A
 W--> 126 <400> 6
 127 atgctggtcg tcctcatctt aataaactgc aaaaagctga agtgcttgac 50

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129 <210> SEQ ID NO: 7
130 <211> LENGTH: 702
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <220> FEATURE:
135 <221> NAME/KEY: CDS
136 <222> LOCATION: (1)...(702)
137 <223> OTHER INFORMATION: Tumor necrosis factor alpha (TNFalpha) mRNA
138 coding region
140 <400> SEQUENCE: 7
141 atg agc act gaa agc atg atc cgq gac gtg gag ctg gcc gag gag gcg 48
142 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
143 1 5 10 15
145 ctc ccc aag aag aca ggg ggg ccc cag ggc tcc agg cgg tgc ttg ttc 96
146 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
147 20 25 30
149 ctc agc ctc ttc tcc ctg atc gtg gca ggc gcc acc acg ctc ttc 144
150 Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
151 35 40 45
153 tgc ctg ctg cac ttt gga gtg atc ggc ccc cag agg gaa gag ttc ccc 192
154 Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
155 50 55 60
157 agg gac ctc tct cta atc agc cct ctg gcc cag gca gtc aga tca tct 240
158 Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
159 65 70 75 80
161 tct cga acc ccg agt gac aag cct gta gcc cat gtt gta gca aac cct 288
162 Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
163 85 90 95
165caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc 336
166 Gln Ala Glu Gly Gln Leu Trp Leu Asn Arg Arg Ala Asn Ala Leu
167 100 105 110
169 ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg cca tca 384
170 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
171 115 120 125
173 gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc 432
174 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
175 130 135 140
177 tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc 480
178 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
179 145 150 155 160
181 gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc 528
182 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
183 165 170 175
185 tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag 576
186 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
187 180 185 190
189 ccc atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc 624
190 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
191 195 200 205

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193 agc gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg 672
 194 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 195 210 215 220
 197 cag gtc tac ttt ggg atc att gcc ctg tga 702
 198 Gln Val Tyr Phe Gly Ile Ile Ala Leu *
 199 225 230
 202 <210> SEQ ID NO: 8
 203 <211> LENGTH: 233
 204 <212> TYPE: PRT
 205 <213> ORGANISM: Homo sapiens
 207 <400> SEQUENCE: 8
 208 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 209 1 5 10 15
 210 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 211 20 25 30
 212 Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
 213 35 40 45
 214 Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 215 50 55 60
 216 Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
 217 65 70 75 80
 218 Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 219 85 90 95
 220 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 221 100 105 110
 222 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 223 115 120 125
 224 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 225 130 135 140
 226 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 227 145 150 155 160
 228 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 229 165 170 175
 230 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 231 180 185 190
 232 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 233 195 200 205
 234 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 235 210 215 220
 236 Gln Val Tyr Phe Gly Ile Ile Ala Leu
 237 225 230
 240 <210> SEQ ID NO: 9
 241 <211> LENGTH: 1793
 242 <212> TYPE: DNA
 243 <213> ORGANISM: Homo sapiens
 245 <220> FEATURE:
 246 <221> NAME/KEY: CDS
 247 <222> LOCATION: (74)...(1201)
 248 <223> OTHER INFORMATION: beta-actin expression (ACTB) mRNA coding region

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250 <400> SEQUENCE: 9
251 cgcgtccgcc ccgcgagcac agagcctcgc ctttgcgcgt ccgcgcgcgc tccacacccg 60
252 cgcgcagctc acc atg gat gat gat atc gcc gcg ctc gtc gtc gac aac 109
253 Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn
254 1 5 10
256 ggc tcc ggc atg tgc aag gcc ggc ttc gcg ggc gac gat gcc ccc cgg 157
257 Gly Ser Gly Met Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg
258 15 20 25
260 gcc gtc ttc ccc tcc atc gtg ggg cgc ccc agg cac cag ggc gtg atg 205
261 Ala Val Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met
262 30 35 40
264 gtg ggc atg ggt cag aag gat tcc tat gtg ggc gac gag gcc cag agc 253
265 Val Gly Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser
266 45 50 55 60
268 aag aga ggc atc ctc acc ctg aag tac ccc atc gag cac ggc atc gtc 301
269 Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val
270 65 70 75
272 acc aac tgg gac gac atg gag aaa atc tgg cac cac acc ttc tac aat 349
273 Thr Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn
274 80 85 90
276 gag ctg cgt gtg gct ccc gag gag cac ccc gtg ctg ctg acc gag gcc 397
277 Glu Leu Arg Val Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala
278 95 100 105
280 ccc ctg aac ccc aag gcc aac cgc gag aag atg acc cag atc atg ttt 445
281 Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe
282 110 115 120
284 gag acc ttc aac acc cca gcc atg tac gtt gct atc cag gct gtg cta 493
285 Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu
286 125 130 135 140
288 tcc ctg tac gcc tct ggc cgt acc act ggc atc gtg atg gac tcc ggt 541
289 Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly
290 145 150 155
292 gac ggg gtc acc cac act gtg ccc atc tac gag ggg tat gcc ctc ccc 589
293 Asp Gly Val Thr His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro
294 160 165 170
296 cat gcc atc ctg cgt ctg gac ctg gct ggc cgg gac ctg act gac tac 637
297 His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr
298 175 180 185
300 ctc atg aag atc ctc acc gag cgc ggc tac agc ttc acc acc acg gcc 685
301 Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Ala
302 190 195 200
304 gag cgg gaa atc gtg cgt gac att aag gag aag ctg tgc tac gtc gcc 733
305 Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala
306 205 210 215 220
308 ctg gac ttc gag caa gag atg gcc acg gct gct tcc agc tcc tcc ctg 781
309 Leu Asp Phe Glu Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Leu
310 225 230 235
312 gag aag agc tac gag ctg cct gac ggc cag gtc atc acc att ggc aat 829
313 Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn

VERIFICATION SUMMARY

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L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:58 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:75 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:92 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:109 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:126 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6